PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/487,550*

DATE: 10/10/97
TIME: 08:46:18

INPUT SET: S12522.raw

> This Raw Listing contains the General Information Section and up to the first 5 pages.

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1                                    SEQUENCE LISTING
2
3    (1)    General Information:
4
5        (i) APPLICANT: Anderson, Darrell R.
6
7      (ii) TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
8            TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
9            PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
10           IMMUNOSUPPRESANTS"
11
12    (iii) NUMBER OF SEQUENCES: 12
13
14     (iv) CORRESPONDENCE ADDRESS:
15           (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
16           (B) STREET: 699 Prince Street
17           (C) CITY: Alexandria
18           (D) STATE: VA
19           (E) COUNTRY: USA
20           (F) ZIP: 22314
21
22      (v) COMPUTER READABLE FORM:
23           (A) MEDIUM TYPE: Floppy disk
24           (B) COMPUTER: IBM PC compatible
25           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28     (vi) CURRENT APPLICATION DATA:
29           (A) APPLICATION NUMBER: US 08/487,550
30           (B) FILING DATE: 07-JUN-1995
31           (C) CLASSIFICATION:
32
33   (viii) ATTORNEY/AGENT INFORMATION:
34           (A) NAME: Teskin, Robin L.
35           (B) REGISTRATION NUMBER: 35,030
36           (C) REFERENCE/DOCKET NUMBER: 012712-131
37
38     (ix) TELECOMMUNICATION INFORMATION:
39           (A) TELEPHONE: 703-836-6620
40           (B) TELEFAX: 703-836-2021
41
42
43   (2) INFORMATION FOR SEQ ID NO:1:
44
45       (i) SEQUENCE CHARACTERISTICS:
46           (A) LENGTH: 705 base pairs
```

INPUT SET: S12522.raw

```
47            (B) TYPE: nucleic acid
48            (C) STRANDEDNESS: Not Relevant
49            (D) TOPOLOGY: linear
50
51      (ii) MOLECULE TYPE: peptide
52
53
54      (ix) FEATURE:
55            (A) NAME/KEY: CDS
56            (B) LOCATION: 1..705
57
58      (ix) FEATURE:
59            (A) NAME/KEY: mat_peptide
60            (B) LOCATION: 1..705
61
62
63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65  ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTG CTG CTC TGG CTC CCA      48
66  Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
67   1               5               10                  15
68
69  GGT GCA CGA TGT GCC TAT GAA CTG ACT CAG CCA CCC TCG GTG TCA GTG      96
70  Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val
71               20                  25                  30
72
73  TCC CCA GGA CAG ACG GCC AGG ATC ACC TGT GGG GGA GAC AAC AGT AGA     144
74  Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg
75               35                  40                  45
76
77  AAT GAA TAT GTC CAC TGG TAC CAG CAG AAG CCA GCG CGG GCC CCT ATA     192
78  Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
79       50                  55                  60
80
81  CTG GTC ATC TAT GAT GAT AGT GAC CGG CCC TCA GGG ATC CCT GAG CGA     240
82  Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
83   65                  70                  75                  80
84
85  TTC TCT GGC TCC AAA TCA GGG AAC ACC GCC ACC CTG ACC ATC AAC GGG     288
86  Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
87                   85                  90                  95
88
89  GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGG     336
90  Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
91               100                 105                 110
92
93  GCT AGT GAT CAT CCG GTC TTC GGA GGA GGG ACC CGG GTG ACC GTC CTA     384
94  Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
95               115                 120                 125
96
97  GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT     432
98  Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
99               130                 135                 140
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INPUT SET: S12522.raw

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100
101   GAG GAG CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC        480
102   Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
103   145               150               155               160
104
105   TTC TAC CCG GGA GCC GTG ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC        528
106   Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
107               165               170               175
108
109   GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC        576
110   Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
111               180               185               190
112
113   AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG TGG AAG        624
114   Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
115               195               200               205
116
117   TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG        672
118   Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
119       210               215               220
120
121   GAG AAG ACA GTG GCC CCT ACA GAA TGT TCA TGA                            705
122   Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  *
123   225               230               235
124
125
126   (2) INFORMATION FOR SEQ ID NO:2:
127
128           (i) SEQUENCE CHARACTERISTICS:
129                   (A) LENGTH:  234 amino acids
130                   (B) TYPE: amino acid
131                   (D) TOPOLOGY: linear
132
133           (ii) MOLECULE TYPE: protein
134
135           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
136
137   Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
138    1               5               10               15
139
140   Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val
141               20               25               30
142
143   Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg
144               35               40               45
145
146   Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
147       50               55               60
148
149   Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
150    65               70               75               80
151
152   Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
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INPUT SET: S12522.raw

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153                      85                    90                    95
154
155   Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
156               100                   105                   110
157
158   Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
159         .     115                   120                   125
160
161   Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
162         130                   135                   140
163
164   Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
165   145                   150                   155                   160
166
167   Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
168               165                   170                   175
169
170   Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
171               180                   185                   190
172
173   Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
174         195                   200                   205
175
176   Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
177         210                   215                   220
178
179   Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
180   225                   230                   235
181
182   (2) INFORMATION FOR SEQ ID NO:3:
183
184         (i) SEQUENCE CHARACTERISTICS:
185               (A) LENGTH: 1431 base pairs
186               (B) TYPE: nucleic acid
187               (C) STRANDEDNESS: Not Relevant
188               (D) TOPOLOGY: linear
189
190         (ii) MOLECULE TYPE: peptide
191
192
193         (ix) FEATURE:
194               (A) NAME/KEY: CDS
195               (B) LOCATION: 1..1431
196
197         (ix) FEATURE:
198               (A) NAME/KEY: mat_peptide
199               (B) LOCATION: 1..1431
200
201
202         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
203
204   ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG        48
205   Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
```

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/487,550*

INPUT SET: S12522.raw

```
206      1              5              10             15
207
208  GTC CTG TCC CAG GTG AAG CTG CAG CAG TGG GGC GAA GGA CTT CTG CAG    96
209  Val Leu Ser Gln Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln
210              20             25             30
211
212  CCT TCG GAG ACC CTG TCC CGC ACC TGC GTT GTC TCT GGT GGC TCC ATC   144
213  Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile
214              35             40             45
215
216  AGC GGT TAC TAC TAC TGG ACC TGG ATC CGC CAG ACC CCA GGG AGG GGA   192
217  Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly
218          50             55             60
219
220  CTG GAG TGG ATT GGC CAT ATT TAT GGT AAT GGT GCG ACC ACC AAC TAC   240
221  Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr
222  65                 70             75                 80
223
224  AAT CCC TCC CTC AAG AGT CGA GTC ACC ATT TCA AAA GAC ACG TCC AAG   288
225  Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys
226              85             90             95
227
228  AAC CAG TTC TTC CTG AAC TTG AAT TCT GTG ACC GAC GCG GAC ACG GCC   336
229  Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala
230              100            105            110
231
232  GTC TAT TAC TGT GCG AGA GGC CCT CGC CCT GAT TGC ACA ACC ATT TGT   384
233  Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys
234          115            120            125
235
236  TAT GGC GGC TGG GTC GAT GTC TGG GGC CCG GGA GAC CTG GTC ACC GTC   432
237  Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val
238      130            135            140
239
240  TCC TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC   480
241  Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
242  145            150            155            160
243
244  TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG   528
245  Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
246              165            170            175
247
248  GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG   576
249  Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
250              180            185            190
251
252  ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC   624
253  Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
254          195            200            205
255
256  TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC   672
257  Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
258      210            215            220
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/487,550*

INPUT SET: S12522.raw

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423	Stop Codon at end of sequence removed - no error	
562	Stop Codon at end of sequence removed - no error	
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1190	Stop Codon at end of sequence removed - no error	